## SEQUENCE LISTING

- (i) APPLICANT: Rezaie, Alireza
  - Esmon, Charles
- (ii) TITLE OF INVENTION: Calcium Binding Recombinant Antibody
  Against Protein C
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Patrea L. Pabst
  - (B) STREET: 1100 Peachtree Street, Suite 2800
  - (C) CITY: Atlanta
  - (D) STATE: Georgia
  - (E) COUNTRY: USA
  - (F) ZIP: 30309-4530
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE: Jun 9, 1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/982,832
  - (B) FILING DATE: 30-NOV-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)
  - (B) FILING DATE: 12-JUL-1991
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/292,447
  - (B) FILING DATE: 30-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Pabst, Patrea L.
  - (B) REGISTRATION NUMBER: 31,284
  - (C) REFERENCE/DOCKET NUMBER: OMRF106CIP

- '(ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (404) 815-6508
  - (B) TELEFAX: (404) 815-6555
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (v) FRAGMENT TYPE: Internal
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: YES
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

# AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTTGCC

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

### 

- (2) INFORMATION FOR SEQ ID NO:4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: YES
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

# AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

## AGGTTACTCT GCTCGAGTCT GGCCCTGG

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

# AGGCCTACTA GTTTACTAAC AATCCCTGGG CACAAT

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

# TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCCGGC

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 34 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: YES
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

# TCCTTCTAGA TTACTAACAC TCTCCCCTGT TGAA

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 1..57
- (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 57."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION:  $58..\overline{4}17$
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 58 through 417."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGCAGGC	TTTCTTCTTC	ATTCTTGCTA	CTGATTGCCC	CTGCATATGT	CCTGTCCCAG	60
GTTACTCTGA	AAGAGTCTGG	CCCTGGGATA	TTGCAGCCCT	CCCAGACCCT	CACTCTGACT	120
TGTTCTCTCT	CTGGGTTTTC	ACTGAGGACT	TCTGGTATGG	GTGTAGGCTG	GATTCGTCAG	180
CCTTCAGGGA	AGGGTCTGGA	GTGGCTGGCA	CACATTTGGT	GGGATGATGA	CAAGCGCTAT	240
AACCCAGTCC	TGAAGAGCCG	ACTGATAATC	TCCAAGGATA	CCTCCAGGAA	ACAGGTATTC	300
CTCAAGATCG	CCAGTGTGGA	CACTGCAGAT	ACTGCCACAT	ACTACTGTGT	TCGAATGATG	360
GATGATTACG	ACGCTATGGA	CTACTGGGGT	CAAGGAACCT	CAGTCACCGT	CTCCTCT	417

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 139 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (v) FRAGMENT TYPE: Internal
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 20..139
- (D) OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala Tyr 1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
20 25 30

Pro Ser Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser Gly Phe Ser Leu 35 40 45

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr 65 70 75 80

Asn Pro Val Leu Lys Ser Arg Leu Ile Ile Ser Lys Asp Thr Ser Arg 85 90 95 Lys Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
Thr Tyr Tyr Cys Val Arg Met Met Asp Asp Tyr Asp Ala Met Asp Tyr
115 Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 387 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa) .
    - (ix) FEATURE:
      - (A) NAME/KEY: misc feature
      - (B) LOCATION:  $1..6\overline{6}$
- (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 66."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 67..387
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 67 through 387."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGATTTTC AGGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCCTCAGT CATAATGTCC 60

AGAGGACAAA TTATTCTCAC CCAGTCTCCG GCAATCATGT CTGCATCTCT GGGGGAGGAG 120

ATCACCCTAA CCTGCAGTGC CACTTCGAGT GTAACTTACG TCCACTGGTA CCAGCAGAAG 180

TCAGGCACT'	r cr	CCCA	AACT	CTT	GATT'	ГАТ	GGGA	CATC	CA A	CCTG	GCTT	C TG	GAGT	CCCT		240
TCTCGTTTC.	A GT	GGCA	GTGG	GTC	TGGG	ACC	TTTT	ATTC:	гс т	CACA	GTCA	G CA	GTGT	GGAĞ		300
GCTGAAGAT	G CT	GCCG.	ATTA	TTA	CTGC	CAT	CAGT	GGAA'	ra G	TTAT	CCGC	A CA	CGTT	CGGA		360
GGGGGGACC	A AG	CTGG	AAAT	AAA	ACGG											387
(ii) (iii) (iv)	SEQU (A) (B) (C) (D) MOLE HYPO ANTI FRAG (A) (A)	ENCE LEN TYP STR TOP CULE THET -SEN MENT INAL ORG	CHA GTH: E: a ANDE OLOG TYP ICAL SE: TYP SOU ANIS	RACT 129 mino DNES Y: 1 PE: p NO PE: N PE: N PE: N PE: N PE: N	ERIS ami aci S: s inea epti  -ter	TICS no a d ingl r de mina Lic feat	acids Le al ght C	hain							opa) cs ma	ture
peptide.' (xi)	SEQU	JENCE	E DES	CRIE	PTION	r: S	EQ II	NO:	12:							
Met 1	Asp	Phe	Gln	Val 5	Gln	Ile	Phe	Ser	Phe 10	Leu	Leu	Ile	Ser	Ala 15	Ser	
Val	Ile	Met	Ser 20	Arg	Gly	Gln	Ile	Ile 25	Leu	Thr	Gln	Ser	Pro 30	Ala	Ile	
Met	Ser	Ala 35	Ser	Leu	Gly	Glu	Glu 40	Ile	Thr	Leu	Thr	Cys 45	Ser	Ala	Thr	

Ser Ser Val Thr Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Thr Ser 50 55 60

Pro Lys Leu Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr Val 85 90 95

Ser Ser Val Glu Ala Glu Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp 100 105 110

Asn Ser Tyr Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 115 120 125

Arg

# SEQUENCE LISTING



# (1) GENERAL INFORMATION:

- Rezaie, Alireza Esmon, Charles (i) APPLICANT:
- Calcium Binding Recombinant Antibody Against Protein C (ii) TITLE OF INVENTION:
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
- ADDRESSEE: Patrea L. Pabst
- Suite 2800 STREET: 1100 Peachtree Street,
  - CITY: Atlanta Ω

B

- STATE: Georgia <u>(a</u>
  - COUNTRY: USA (E)
- ZIP: 30309-4530
- (v) COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy disk (A)
- (B)
- OPERATING SYSTEM: PC-DOS/MS-DOS COMPUTER: IBM PC compatible ပြ
- SOFTWARE: PatentIn Release #1.0, Version #1.25 <u>(a)</u>
- CURRENT APPLICATION DATA: (vi)
- (A) APPLICATION NUMBER: US
- FILING DATE: (B)
- CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/982,832 (B) FILING DATE: 30-NOV-1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)

- (B) FILING DATE: 12-JUL-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/292,447 (B) FILING DATE: 30-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAMÉ: Pabst, Patrea L.(B) REGISTRATION NUMBER: 31,284(C) REFERENCE/DOCKET NUMBER: OMRF106CIP
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (404) 815-6508
  - (B) TELEFAX: (404) 815-6555
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids (B) TYPE: amino acid
- STRANDEDNESS: single (C)
  - TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- - (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: Internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys 1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 40 base pairs

TYPE: nucleic acid STRANDEDNESS: single (B) TYPE: nucleic aci (C) STRANDEDNESS: sir (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTTGCC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGCGGCCGC CCCCCCCC CCCCCCCCC

(2) INFORMATION FOR SEQ ID NO:4:

40

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

TYPE: nucleic acid (B) TYPE: nucleic act (C) STRANDEDNESS: sin (D) TOPOLOGY: linear

STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

STRANDEDNESS: single (B) TYPE: nucleic acid (C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGTTACTCT GCTCGAGTCT GGCCCTGG

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

40

28

LENGTH: 36 base pairs 

STRANDEDNESS: single TYPE: nucleic acid

TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGCCTACTA GTTTACTAAC AATCCCTGGG CACAAT

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs (B)

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear (O)

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCCGGC

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 34 base pairs (i) SEQUENCE CHARACTERISTICS:

37

S

- TYPE: nucleic acid STRANDEDNESS: single (B) TYPE: nucleic ac.(C) STRANDEDNESS: sin(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCTTCTAGA TTACTAACAC TCTCCCCTGT TGAA

34

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
- FEATURE: (ix)
- (A) NAME/KEY: misc\_feature (B) LOCATION: 1..57 (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through

57."

(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 58417	יייסיים אל יייסיים בייים
OIDER	2
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
ITGGGCAGGC TTTCTTCTTC ATTCTTGCTA CTGATTGCCC CTGCATATGT CCTGTCCCAG	09
FITACTCTGA AAGAGTCTGG CCCTGGGATA TTGCAGCCCT CCCAGACCCT CACTCTGACT	120
GTTCTCTCT CTGGGTTTTC ACTGAGGACT TCTGGTATGG GTGTAGGCTG GATTCGTCAG	180
CCTTCAGGGA AGGGTCTGGA GTGGCTGGCA CACATTTGGT GGGATGATGA CAAGCGCTAT	240
AACCCAGTCC TGAAGAGCCG ACTGATAATC TCCAAGGATA CCTCCAGGAA ACAGGTATTC	300
TCAAGATCG CCAGTGTGGA CACTGCAGAT ACTGCCACAT ACTACTGTGT TCGAATGATG	360
ATGATTACG ACGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCT	417
2) INFORMATION FOR SEQ ID NO:10:	
(i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 139 amino acids     (B) TYPE: amino acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(iii) HYPOTHETICAL: NO	,
(iv) ANTI-SENSE: NO	
/v/ FRACMENT TVDF. Internal	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)

FEATURE: (ix)

(A) NAME/KEY: misc feature(B) LOCATION: 20..139(D) OTHER INFORMATION: /not

OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala 1 Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln 25 Val Leu Ser

Gly Phe Ser Leu 45 Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser 40

Lys G1yGln Pro Ser 60 Gly Trp Ile Arg Val 55 Gly Gly Met Ser

Thr 50

Arg

Ser

Pro

Tyr 80 Arg Trp Trp Asp Asp Asp Lys Ile Gly Leu Glu Trp Leu Ala His 65

Arg Ser Ser Arg Leu Ile Ile Ser Lys Asp Thr Asn Pro Val Leu Lys 85

Thr Ala Asp | 110 Ser Val Asp Thr Ala 105 Phe Leu Lys Ile Ala 100 Lys Gln Val

TyrTyr Asp Ala Met Asp 125 Met Asp Asp 120 Arg Met Cys Val Tyr115 TyrThr

Ser Thr Val Ser Trp Gly Gln Gly Thr Ser Val 130

(2) INFORMATION FOR SEQ 1D NO:11:
(i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 387 base pairs     (B) TYPE: nucleic acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE: (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)
<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION: 166     (C) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through (D) OTHER INFORMATION: /note="Signal peptide encoded by nucleotides 1 through (D) OTHER INFORMATION: /note="Signal peptide")</pre>
<ul> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: misc feature</li> <li>(B) LOCATION: 67387</li> <li>(D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 67 through 387."</li> </ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
ATGGATTTTC AGGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCCTCAGT CATAATGTCC 60
AGAGGACAAA TTATTCTCAC CCAGTCTCCG GCAATCATGT CTGCATCTCT GGGGGGGGG
ATCACCCTAA CCTGCAGTGC CACTTCGAGT GTAACTTACG TCCACTGGTA CCAGCAGAAG 180

TCAGGCAC	TCAGGCACTT CTCCCAAACT CTTGATTTAT GGGACATCCA ACCTGGCTTC TGGAGTCCCT 24	240
TCTCGTTT	TCTCGTTTCA GTGGCAGTGG GTCTGGGACC TTTTATTCTC TCACAGTCAG CAGTGTGGAG	300
GCTGAAGATG	CTGCCGATTA TTACTGCCAT CAGTGGAATA GTTATCCGCA CACGTTCGGA	360
GGGGGGAC	GGGGGGCCCA AGCTGGAAAT AAAACGG	387
(2) INFO	(2) INFORMATION FOR SEQ ID NO:12:	
(i)	(i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 129 amino acids     (B) TYPE: amino acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear	
(ii)	(ii) MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(iv)	ANTI-SENSE: NO	
(v)	FRAGMENT TYPE: N-terminal	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)	
(ix)	FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 23129 (D) OTHER INFORMATION: /note= "Gln at position 23 starts mature	re peptid
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:12:	
Met 1	Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser $1$	

Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro 70Val Ile Met Ser Arg Gly Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile 20 30 Ala Ser Leu Gly Glu Glu Ile Thr Leu Thr Cys Ser Ala Thr 35 45 Val Tyr Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 115 Glu Ala Glu Asp Ala Asp Tyr Tyr Cys His Gln Trp 100 110 Trp Tyr Gln Gln Lys Ser Gly Thr 60 Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr 90 His ' 55 Ser Val Thr Tyr Val 50 Pro Lys Leu Leu Ile 65 Ser Arg Phe Ser Gly 85 Ser Ser Val Ser Asn Ser Ser Met

Arg